

# Morteza Sabri

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[Portfolio](#) | [LinkedIn](#) | [Github](#) | [GoogleScholar](#) | [Orcid](#)

## PROFESSIONAL SUMMARY

Experienced bioinformatician specializing in bulk and single-cell RNA-Seq analysis—applied to cardiovascular and neurodevelopment research—proficient in R, Shell, and HPC. Developed pipelines accelerating analysis by 80%, identifying novel biomarkers, boosting productivity and reproducibility. Passionate about teaching and solving biological problems through bioinformatics. For more about my background and selected projects, please see my portfolio: <https://mortezasabri.github.io/>

## HIGHLIGHTED AREAS OF EXPERTISE

- Bulk & single-cell RNA-Seq
- Data Visualization & Reproducibility
- R programming & Shell Scripting
- Study design & Data Interpretation

## EXPERIENCE

### Scientific Staff, Bioinformatician | RWTH Aachen University, Aachen Jan 2025 – Apr 2025

- Performed single-cell RNA-Seq analysis to study neuron migration in the absence of DNMT1.
- Conducted methylation array data analysis on 64 subjects with postpartum depression.
- Handled data preprocessing (Parse Bioscience's Trailmaker), statistical analysis, and visualization (R).

### Scientific Staff, Bioinformatician | Technical University of Munich, Munich Nov 2023 - Nov 2024

- Conducted bulk and single-cell RNA-Seq analyses for cardiovascular research.
- Managed workflows from raw data to functional interpretation and identifying new biomarkers.
- Generated publication-ready visualizations illustrating gene-disease associations.
- Optimized preprocessing pipelines with R/Shell scripting, reducing runtime up to 80%.

### Guest Scientist, Bioinformatician | Helmholtz Munich, Munich Oct 2024 - Nov 2024

- Performed deconvolution analysis to interpret bulk RNA-Seq datasets using BayesPrism R package to elucidate cell-type composition.

### Instructor & Freelance, Bioinformatician | Self-Employed, Tehran 2019 – 2022

- Delivered over 10 onsite workshops on R programming, RNA-Seq, and Linux/Shell scripting.
- Provided freelance bioinformatics services including RNA-Seq, epigenomics, and visualization.
- Supported manuscript revisions by performing advanced statistical analyses (e.g., MINT).
- Hosted Biocast101 podcast ([Apple](#), [Spotify](#), [Castbox](#), [PodLink](#)).
- Created contents on social media known as Bioinformatics101 ([YouTube](#), [Instagram](#), etc).

## SKILLS

### Laboratory Techniques:

- RNA/DNA Extraction
- PCR & qRT-PCR
- Primer Design

### Programming Languages:

- R
- Shell/Bash
- Markdown & LaTeX
- Git & GitHub
- MATLAB (Basic)
- Python (Basic)

### Bioinformatics Workflows:

- Bulk & single-cell RNA-seq
- ChIP-Seq

- Genome Assembly
- Expression & Methylation Arrays

### Software and HPC:

- CLC Genomics Workbench
- Galaxy
- Jupyter Lab
- SPSS & GraphPad Prism
- Sherlock & RWTH Aachen cluster

### Transferable & Soft Skills

- Paper Writing
- Teaching & Mentoring: Tutorials & Workshops
- Open Science & Reproducibility
- FAIR Data Principles & Metadata Standards
- Teamwork & Communication

## EDUCATION

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**M.Sc. Biology (Genetics), University of Sistan and Baluchestan, Iran**

- **Thesis:** "Investigation of Superoxide Dismutase and Catalase Gene Expression under Drought Stress: A Comparative Study between Sistan and Baluchestan and Moderate Cultivars".

**B.Sc. Cellular and Molecular Biology (Genetics), Islamic Azad University, Iran**

## CERTIFICATIONS & LANGUAGES

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**TOEFL iBT**, ETS - Score: 110, February 2023

**Languages:** Persian (Native), English (Proficient), Azeri (Basic)

## PUBLICATION

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Overcoming trastuzumab resistance in HER2-positive breast cancer, Journal of Cellular Physiology, 2019.

[DOI: 10.1002/jcp.29216](https://doi.org/10.1002/jcp.29216)

Evaluation of monolignol biosynthesis gene network in Camelina sativa, Agricultural Biotechnology Journal, 2020.

Investigation of Superoxide Dismutase and Catalase Gene Expression under Drought Stress: A Comparative Study between Sistan and Baluchestan and Moderate Cultivars – (Draft)

## TEACHING EXPERIENCE

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Workshops: R & Linux/Shell programming, RNA-Seq, Visualization and basic stats in R

[Certificates and materials on my portfolio](#)

## HIGHLIGHTED PIPELINES

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- Bulk RNA-Seq (STAR/HISAT2 → DESeq2/edgeR → GO/KEGG)
- scRNA-Seq (Seurat & SingleCellExperiment)
- Genome assembly (Velvet, SPAdes)
- Epigenomic analyses (minfi and limma on IDAT files)

[More details on my portfolio](#)

## INTERESTS

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Genome editing, Machine learning, Comparative genomics, Data science, Computer science

Climbing, Hiking, Camping, Mountaineering

## REFERENCE

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Prof. Dr. Lars Mägdefessel

Dr. Mahboubeh Yazdanifar

Dr. Komeil Razmi

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